

SEQUENCE LISTING

<110> DOI, Hirofumi
KUDO, Gen

<120> Method of Degradation, Method for Inhibiting Degradation,
and Agent for Inhibiting Degradation, for Transcription
Factors of Glucose Metabolism-Related Genes

<130> 3190-072

<140> US Unassigned
<141> 2005-02-28

<150> PCT/JP2003/11046
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<150> JP P2003-96371
<151> 2003-03-31

<150> JP P2003-96372
<151> 2003-03-31

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<170> PatentIn version 3.1

<210> 1
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<212> PRT
<213> Homo sapiens

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Met Asp Met Ala Asp Tyr Ser Ala Ala Leu Asp Pro Ala Tyr Thr Thr
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Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met Gly Asn Asp Thr Ser
20 25 30

Pro Ser Glu Gly Thr Asn Leu Asn Ala Pro Asn Ser Leu Gly Val Ser
35 40 45

Ala Leu Cys Ala Ile Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly
50 55 60

Ala Ser Ser Cys Asp Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg
65 70 75 80

Lys Asn His Met Tyr Ser Cys Arg Phe Ser Arg Gln Cys Val Val Asp
85 90 95

Lys Asp Lys Arg Asn Gln Cys Arg Tyr Cys Arg Leu Lys Lys Cys Phe
100 105 110

Arg Ala Gly Met Lys Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile
115 120 125

Ser Thr Arg Arg Ser Ser Tyr Glu Asp Ser Ser Leu Pro Ser Ile Asn
130 135 140

Ala Leu Leu Gln Ala Glu Val Leu Ser Arg Gln Ile Thr Ser Pro Val
145 150 155 160

Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys Lys Ile Ala Ser Ile Ala
165 170 175

Asp Val Cys Glu Ser Met Lys Glu Gln Leu Leu Val Leu Val Glu Trp
180 185 190

Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro Leu Asp Asp Gln Val
195 200 205

Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Ala Thr
210 215 220

Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu Gly Asn Asp Tyr
225 230 235 240

Ile Val Pro Arg His Cys Pro Glu Leu Ala Glu Met Ser Arg Val Ser
245 250 255

Ile Arg Ile Leu Asp Glu Leu Val Leu Pro Phe Gln Glu Leu Gln Ile
260 265 270

Asp Asp Asn Glu Tyr Ala Tyr Leu Lys Ala Ile Ile Phe Phe Asp Pro
275 280 285

Asp Ala Lys Gly Leu Ser Asp Pro Gly Lys Ile Lys Arg Leu Arg Ser
290 295 300

Gln Val Gln Val Ser Leu Glu Asp Tyr Ile Asn Asp Arg Gln Tyr Asp
305 310 315 320

Ser Arg Gly Arg Phe Gly Glu Leu Leu Leu Leu Pro Thr Leu Gln
325 330 335

Ser Ile Thr Trp Gln Met Ile Glu Gln Ile Gln Phe Ile Lys Leu Phe
340 345 350

Gly Met Ala Lys Ile Asp Asn Leu Leu Gln Glu Met Leu Leu Gly Gly
355 360 365

Ser Pro Ser Asp Ala Pro His Ala His His Pro Leu His Pro His Leu
370 375 380

Met Gln Glu His Met Gly Thr Asn Val Ile Val Ala Asn Thr Met Pro
385 390 395 400

Thr His Leu Ser Asn Gly Gln Met Cys Glu Trp Pro Arg Pro Arg Gly
405 410 415

Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro Ser Pro Pro Gly Gly Ser
420 425 430

Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val
435 440 445

Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val
450 455 460

Ile
465

<210> 2
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<213> Homo sapiens

<220>
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<222> (322)..(322)

<223> UNSURE

Xaa may be Tyr since it has been shown in many reports
that the codon of Xaa is tat.

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Met Val Ser Lys Leu Ser Gln Leu Gln Thr Glu Leu Leu Ala Ala Leu
1 5 10 15

Leu Glu Ser Gly Leu Ser Lys Glu Ala Leu Ile Gln Ala Leu Gly Glu
20 25 30

Pro Gly Pro Tyr Leu Leu Ala Gly Glu Gly Pro Leu Asp Lys Gly Glu
35 40 45

Ser Cys Gly Gly Gly Arg Gly Glu Leu Ala Glu Leu Pro Asn Gly Leu
50 55 60

Gly Glu Thr Arg Gly Ser Glu Asp Glu Thr Asp Asp Asp Gly Glu Asp
65 70 75 80

Phe Thr Pro Pro Ile Leu Lys Glu Leu Glu Asn Leu Ser Pro Glu Glu
85 90 95

Ala Ala His Gln Lys Ala Val Val Glu Thr Leu Leu Gln Glu Asp Pro
100 105 110

Trp Arg Val Ala Lys Met Val Lys Ser Tyr Leu Gln Gln His Asn Ile
115 120 125

Pro Gln Arg Glu Val Val Asp Thr Thr Gly Leu Asn Gln Ser His Leu
130 135 140

Ser Gln His Leu Asn Lys Gly Thr Pro Met Lys Thr Gln Lys Arg Ala
145 150 155 160

Ala Leu Tyr Thr Trp Tyr Val Arg Lys Gln Arg Glu Val Ala Gln Gln
165 170 175

Phe Thr His Ala Gly Gln Gly Gly Leu Ile Glu Glu Pro Thr Gly Asp
180 185 190

Glu Leu Pro Thr Lys Lys Gly Arg Arg Asn Arg Phe Lys Trp Gly Pro
 195 200 205

Ala Ser Gln Gln Ile Leu Phe Gln Ala Tyr Glu Arg Gln Lys Asn Pro
 210 215 220

Ser Lys Glu Glu Arg Glu Thr Leu Val Glu Glu Cys Asn Arg Ala Glu
 225 230 235 240

Cys Ile Gln Arg Gly Val Ser Pro Ser Gln Ala Gln Gly Leu Gly Ser
 245 250 255

Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg
 260 265 270

Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly
 275 280 285

Pro Pro Pro Gly Pro Gly Pro Gly Pro Ala Leu Pro Ala His Ser Ser
 290 295 300

Pro Gly Leu Pro Pro Pro Ala Leu Ser Pro Ser Lys Val His Gly Val
 305 310 315 320

Arg Xaa Gly Gln Pro Ala Thr Ser Glu Thr Ala Glu Val Pro Ser Ser
 325 330 335

Ser Gly Gly Pro Leu Val Thr Val Ser Thr Pro Leu His Gln Val Ser
 340 345 350

Pro Thr Gly Leu Glu Pro Ser His Ser Leu Leu Ser Thr Glu Ala Lys
 355 360 365

Leu Val Ser Ala Ala Gly Gly Pro Leu Pro Pro Val Ser Thr Leu Thr
 370 375 380

Ala Leu His Ser Leu Glu Gln Thr Ser Pro Gly Leu Asn Gln Gln Pro
 385 390 395 400

Gln Asn Leu Ile Met Ala Ser Leu Pro Gly Val Met Thr Ile Gly Pro
 405 410 415

Gly Glu Pro Ala Ser Leu Gly Pro Thr Phe Thr Asn Thr Gly Ala Ser
420 425 430

Thr Leu Val Ile Gly Leu Ala Ser Thr Gln Ala Gln Ser Val Pro Val
435 440 445

Ile Asn Ser Met Gly Ser Ser Leu Thr Thr Leu Gln Pro Val Gln Phe
450 455 460

Ser Gln Pro Leu His Pro Ser Tyr Gln Gln Pro Leu Met Pro Pro Val
465 470 475 480

Gln Ser His Val Thr Gln Ser Pro Phe Met Ala Thr Met Ala Gln Leu
485 490 495

Gln Ser Pro His Ala Leu Tyr Ser His Lys Pro Glu Val Ala Gln Tyr
500 505 510

Thr His Thr Gly Leu Leu Pro Gln Thr Met Leu Ile Thr Asp Thr Thr
515 520 525

Asn Leu Ser Ala Leu Ala Ser Leu Thr Pro Thr Lys Gln Val Phe Thr
530 535 540

Ser Asp Thr Glu Ala Ser Ser Glu Ser Gly Leu His Thr Pro Ala Ser
545 550 555 560

Gln Ala Thr Thr Leu His Val Pro Ser Gln Asp Pro Ala Gly Ile Gln
565 570 575

His Leu Gln Pro Ala His Arg Leu Ser Ala Ser Pro Thr Val Ser Ser
580 585 590

Ser Ser Leu Val Leu Tyr Gln Ser Ser Asp Ser Ser Asn Gly Gln Ser
595 600 605

His Leu Leu Pro Ser Asn His Ser Val Ile Glu Thr Phe Ile Ser Thr
610 615 620

Gln Met Ala Ser Ser Ser Gln
625 630

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 <212> PRT
 <213> Homo sapiens

<400> 3

Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp
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Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro
 20 25 30

Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro His
 35 40 45

Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp
 50 55 60

Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala
 65 70 75 80

His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro
 85 90 95

Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro
 100 105 110

Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His
 115 120 125

Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu
 130 135 140

Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu
 145 150 155 160

Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg
 165 170 175

Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile
 180 185 190

Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys
 195 200 205

Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu
 210 215 220

Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro
 225 230 235 240

Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala
 245 250 255

Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser
 260 265 270

Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg
 275 280

<210> 4
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 <223> Partial peptide of human m-calpain or rabbit m-calpain, showing high
 score in the local alignment between human m-calpain or rabbit
 m-calpain and human HNF-4alpha

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Phe Lys Leu Pro Pro Gly
 1 5

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 local alignment between human m-calpain or rabbit m-calpain and
 human HNF-4alpha

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Tyr Lys Leu Leu Pro Gly
 1 5